



# Hairy root culture technology: applications, constraints and prospect

Saikat Gantait<sup>1</sup> · Eashan Mukherjee

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## Abstract

Hairy root (HR) culture, a successful biotechnology combining in vitro tissue culture with recombinant DNA machinery, is intended for the genetic improvement of plants. This technology has been put to use since the last three decades for genetic advancement of medicinal and aromatic plants and also to harvest the economical products in the form of secondary metabolites that are significantly important for their ethnobotanical and pharmacological properties. It also provides an efficient way out for the quicker extraction and quantification of the valuable phytochemicals. The current review provides an account of the in vitro HR culture technology and its wide-scale applications in the field of research as well as in pharmaceutical industries. Different facets of HR with respect to the culture establishment, phytochemical production as well as research investigations concerning the areas of gene manipulation, biotransformation of the secondary metabolites, phytoremediation, their industrial utilisations and different problems encountered during the application of this technology have been covered in this appraisal. Eventually, an idea has been provided on HR about the recent trends on the progress of this technology that may open up newer prospects in near future and calls for further research and explorations in this field.

## Key points

- Genetic engineering–based HR culture aims towards enhanced secondary metabolite production.
- This review explores an insight in the HR technology and its multi-faceted approaches.
- Up-to-date ground-breaking research applications and constraints of HR culture are discussed.

**Keywords** Biotransformation · Genetic engineering · In vitro regeneration · Phytoremediation · Secondary metabolites

## Introduction

Hairy root (HR) culture technology is a novel biotechnological approach that aims towards the genetic and biochemical improvement of various important medicinal plants (Gantait et al. 2020). An array of secondary metabolites is found in different plants with medicinal value. Alkaloids, tannins, flavonoids, phenolics and other aromatic amino acid derivatives constitute the major bulk of these phytobiochemicals. Naturally, these biochemicals are biosynthesised through

different metabolic pathways in plants involving different enzymes or their complexes. These secondary metabolites are found in multiple plant parts such as floral buds, leaves, barks, seeds and, most importantly, in the roots. Extraction of these useful biochemicals (that have remarkable pharmacological, medicinal and ethnobotanical uses) through conventional field-grown methods would involve large-scale uprooting of the plants and, hence, inevitable destruction of their habitat, ecosystem and biodiversity. Such approach has pushed these plants towards endangered category. To mitigate this problem, in vitro culture technology could effectively be applied for the large-scale propagation, conservation as well as production of secondary metabolites from these plants (Gantait et al. 2011; Gangopadhyay et al. 2016; Panigrahi et al. 2018; Verma et al. 2018; Mukherjee et al. 2020). In this scenario, HR culture technology also presents itself as a potential solution to the above-mentioned problem via production and enhancement of secondary metabolite content of these plants (Mitra et al. 2020; Das et al. 2020). These HR cultures could be then

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Saikat Gantait and Eashan Mukherjee contributed equally to this work.

✉ Saikat Gantait  
saikatgantait@yahoo.com

<sup>1</sup> Crop Research Unit (Genetics and Plant Breeding), Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal 741252, India

further employed in pharmaceutical research and product development.

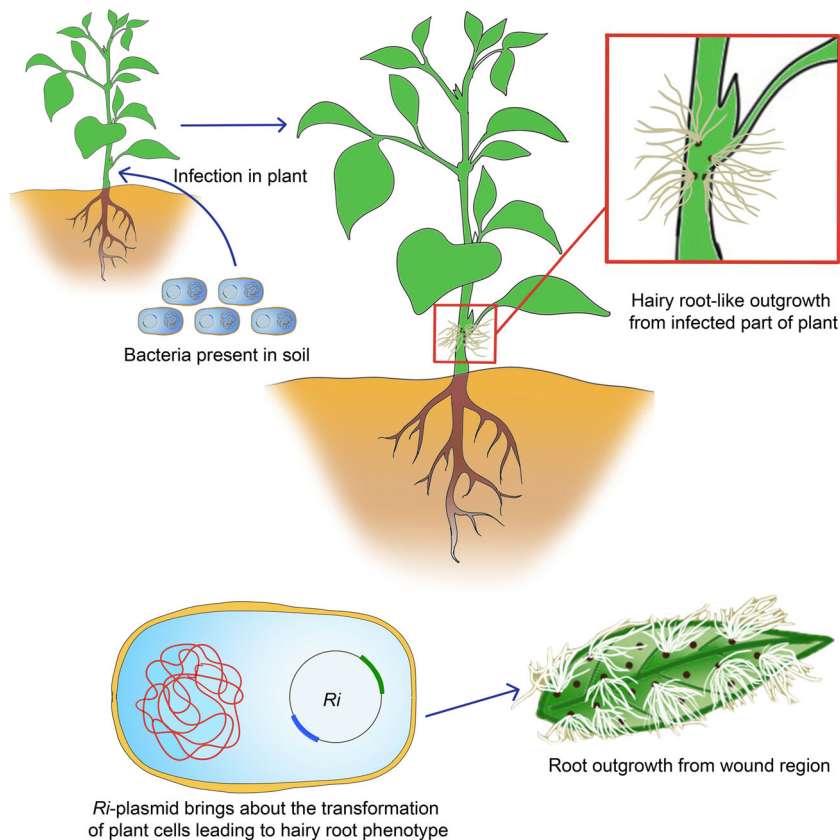
The early 1980s marks the inception of the *in vitro* culture studies of this technology (Willmitzer et al. 1982). HR culture technology mainly involves the use of the soil-inhabiting gram-negative bacteria *Agrobacterium rhizogenes* (Fig. 1). Bacterial cells contain a typical plasmid, called ‘*Ri*-plasmid’ (root-inducing plasmid). During the bacterial infection at the wounded parts of plants, the host plant cells are transformed upon integration of the transfer DNA (T-DNA) segments from the bacteria into its genome (Fig. 2) (Chilton et al. 1982). This transformation is effected owing to the presence of different genes (*rol* genes, i.e. *rol A*, *rol B* and *rol C*) in the plasmid of the bacteria. Upon incorporation, the different genes present in the T-DNA are encoded, and as a result, auxin and cytokinins are produced (Fig. 2) that stimulate the production of HR-like outgrowths from the wounded regions (Shanks and Morgan 1999; Sevón and Oksman-Caldentey 2002; Guillon et al. 2006). On the basis of opine production, *A. rhizogenes* strains are of five types: octopine, mannopine, cucumopine, agropine and nopaline (Zhou et al. 1998), of which agropine strains serve as the preferred choice due to their greater root induction ability. Opine synthesising genes are located in the right border of T-

DNA. In homology to the *tms1* and *tms2* of *Ti* plasmid, the TR-DNA contains genes for auxin production, viz. *Tms1* and *Tms2* (Rawat et al. 2019). Resultant HR typifies quick proliferative phytohormone-independent growth, increased biomass and stable genetic performance with respect to secondary metabolite production. This bacterium, i.e. *A. rhizogenes*, also employs binary vector systems where the genes could be carried on another plasmid inside the cell (Tepfer 1984; Christey 1997). Further investigations in this field over years have led to diversified applications such as phytoremediation and biotransformation, which are further elaborated in this review.

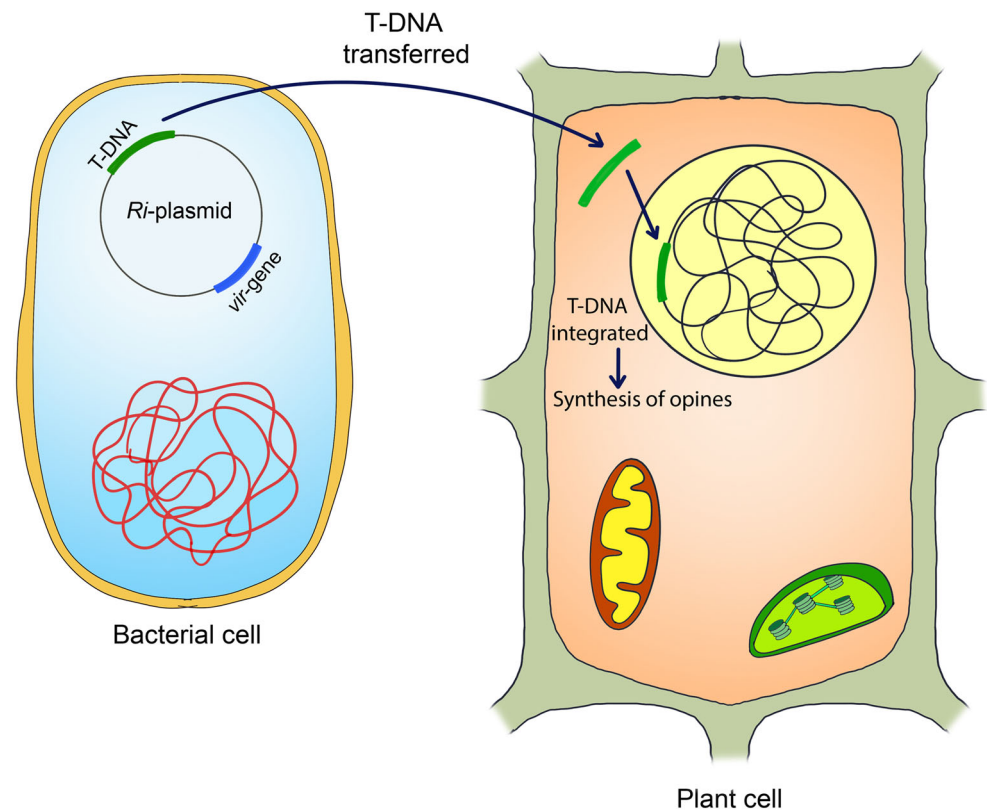
## Techniques involved

For efficient development of HR cultures, various factors like explant type and growth stage, culture conditions, bacterial strains, suitable media for co-cultivations, pH of the medium and carbon source must be mulled over as these factors influence the secondary metabolite biosynthesis. In general, a range of explants like protoplast, leaf, cotyledons, hypocotyls, shoot tips, stem, stalk, storage root and tubers could be employed (Mugnier 1988; Han et al. 1993; Drewes and Staden 1995; Giri et al. 2001b; Krolicka et al.

**Fig. 1** Diagrammatic representation of *Agrobacterium rhizogenes*-mediated hairy root induction in plants under natural conditions (*in vivo*) (Source: unpublished diagram of Saikat Gantait)



**Fig. 2** Diagrammatic representation of the cellular mechanism of *Agrobacterium rhizogenes*-mediated transformation of the host cell (Source: unpublished diagram of Saikat Gantait)

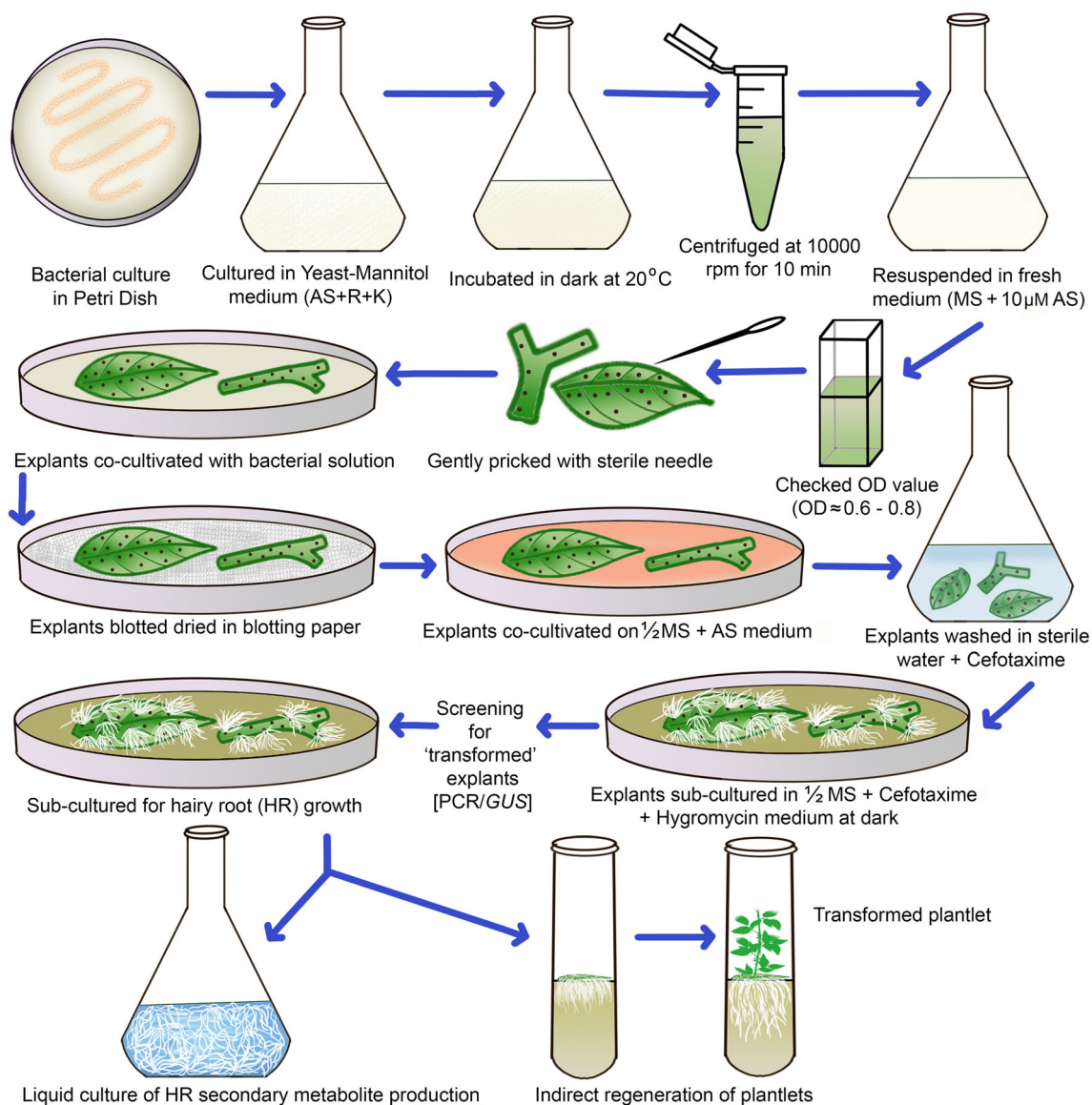


2001; Azlan et al. 2002). In most cases, young and juvenile explants are preferred though, in some cases, it is species dependent (Hu and Du 2006). The explants were initially wounded using a sterile scalpel or needle and then inoculated with bacterial solutions (Fig. 3). Then, explants are co-cultivated in a semisolid medium supplemented with suitable antibiotics such as carbenicillin disodium, cefotaxime sodium, streptomycin sulphate, ampicillin sodium or tetracycline with doses ranging from 100 to 500  $\mu\text{g/ml}$ . This is performed to remove the excess bacteria present on explant surface (Spano et al. 1988; Drewes and Staden 1995; Giri et al. 2001b; Krollicka et al. 2001). Root induction from the wounded places occurs within 7 to 30 days. Subsequent subculturing is done in plant growth regulator (PGR)-free medium (Fig. 3). The media supplemented with heavy metal ions of nitrate, ammonia, phosphate and other elicitors (Payne et al. 1987; Toivonen et al. 1991; Christen et al. 1992; Sevon et al. 1992) promote secondary metabolism in the cultures. Culture conditions like light, temperature, pH and different PGR concentrations added to the basal media chiefly influence secondary metabolite production (Christen et al. 1992; Toivonen et al. 1992; Rhodes et al. 1994; Arroo et al. 1995; Bhadra and Shanks 1995; Vanhala et al. 1998; Morgan et al. 2000).

Reporter genes such as *GUS* gene ( $\beta$ -glucuronidase) (Hosoki and Kigo 1994), kanamycin-resistant enzyme encoded by *NPT-II* gene (neomycin phosphotransferase II) (Han et al. 1993; Qin et al. 1994) and green fluorescent protein

(*GFP*) encoding gene (in *Catharanthus roseus* L. experiments by Hughes et al. 2002) are the most commonly used ones.

In several published reports, it was mentioned that the improvement in the secondary metabolite production could be effected by a range of different approaches such as precursor feeding, cell permeabilisation and elicitation through the use of different agents like detergents, sonication, calcium chelators, temperature and oxygen stress. The usage of the above-mentioned techniques are found in the reports of Thimmaraju et al. (2003a, b) and Moreno-Valenzuela et al. (2003) describing the production of betalaine from beet root and serpentine from *Catharanthus roseus* HR cultures, respectively. Notably, the usage of chitosan, methyl jasmonate (MeJa) and vanadyl sulphate elicitors in case of *Panax ginseng* stimulated ginsenoside production (Palazon et al. 2003a), whereas *Phytophthora cinnamoni* elicitors stimulated harmine and harmaline in case of *Oxalis tuberosa* (Bais et al. 2003). The use of trapping agents such alumina and silica (1:1) in beet root HR cultures in order to enhance betalaine production was reported by Thimmaraju et al. (2004). Cross-species co-culturing method for podophyllotoxin from *Podophyllum hexandrum* using coniferin from *Linum flavum* as precursor was mentioned in the reports of Lin et al. (2003b). Usage of elicitors like  $\text{CuSO}_4$ , MeJa in *Pharbitis nil* for umbelliferone and scopoletin production (Yaoya et al. 2004), *Rhizoctonia bataticola*,  $\beta$ -cyclodextrin and MeJa elicitors in *Solanum tuberosum* for sesquiterpene production was also reported



**Fig. 3** Diagrammatic representation of the in vitro protocol for hairy root culture establishment using *Agrobacterium rhizogenes* and regeneration of transformed plantlet (Source: unpublished diagram of Saikat Gantait)

(Komaraiah et al. 2003). Similarly, reports of Furze et al. (1991) mention the use of metal ion elicitation by  $\text{Cu}^{2+}$  and  $\text{Cd}^{2+}$  in case of *Datura stramonium* for sesquiterpenoid phytoalexin production. Later on, Hu and Du (2006) reported the importance of selection of genetically true high metabolite yielding HR lines. This is due to the ambiguity in proper integration of T-DNA into the plant genome which may lead to variations in the secondary metabolite production.

## Applications

Wide-scale research and investigation in this field have facilitated the advancement of varied applications of HR culture technology. Some of the different prospects as explored

in the available reports on HR culture technology are mentioned as follows.

### Source of important secondary metabolites

Different secondary phytochemicals have been isolated using HR culture technology. Some of the notable examples are artemisinin from *Artemisia*, indole alkaloids from *Catharanthus* and *Cinchona*, forskolin from *Coleus*, withanolides from *Withania*, shikonin from *Lithospermum*, diosgenin from *Trigonella*, etc. (Table 1). Likewise, careful maintenance and regular subculturing of *Nicotiana rustica* HR lines stabilised the yield of nicotine at 300 mg/g fresh weight. Similarly, the different published reports regarding the quantification of products of secondary metabolism from

**Table 1** Applications of hairy root culture technology in the production of various secondary metabolites (in past two decades)

Plant species	Detection of gene transformation	Secondary metabolite obtained	Detection/quantification method	References
<i>Panax ginseng</i>	PCR analysis using <i>rol C</i> , <i>aux1</i> , <i>ags</i> and <i>mas1</i>	Ginsenoside	HPLC	Mallof et al. (2001)
<i>Linum flavum</i>	NM	Coniferin	HPLC	Lin et al. (2003a, b)
<i>Rauwolfia micrantha</i>	PCR analysis using <i>rol A</i> primers	Ajmaline, ajmalicine	TLC and HPLC	Sudha et al. (2003)
<i>Papaver somniferum</i>	PCR analysis using <i>rol A</i> , <i>rol B</i> and <i>rol C</i> genes	Morphine, sanguinarine, codeine	HPLC	Le Flem-Bonhomme et al. (2004)
<i>Gynostemma pentaphyllum</i>	PCR analysis using <i>rol B</i> primers	Gypenoside	TLC	Chang et al. (2005)
<i>Gmelina arborea</i>	PCR analysis using <i>rol B</i> -specific primers	Verbascoside	HPLC	Dhakulkar et al. (2005)
<i>Rauwolfia serpentina</i>	PCR analysis using <i>rol A</i> primers	Reserpine	HR culture; NM	Goel et al. (2010)
<i>Bacopa monnieri</i>	PCR detection of TL-DNA and TR-DNA	Bacopasaponin (D and F) and bacopaside (II and V)	HPTLC	Majumdar et al. (2011)
<i>Ageratum conyzoides</i>	PCR analysis using <i>rol C</i> primers	$\beta$ -Farnesene, precocene I and $\beta$ -caryophyllene	Hydro-distillation	Abdelkader and Lockwood (2011)
<i>Taraxacum officinale</i>	NM	Sesquiterpene lactones	HPTLC	Maresh and Jeyachandran (2011)
<i>Verbascum xanthophoeniceum</i>	PCR	Verbascoside	LC-APCI-MS analyses	Georgiev et al. (2011)
<i>Gentiana cruciata</i>	PCR analysis using <i>rol C</i> primers	Gentiopicroside	HPTLC	Hayta et al. (2011)
<i>Picrothiza kurroa</i>	PCR analysis revealed the presence of the <i>rol B</i> genes	Picrotin and picrotoxinin	HPTLC	Mishra et al. (2011)
<i>Hyoscyamus muticus</i>	PCR analysis using <i>rol C</i> primers	Scopolamine and hyoscyamine	GC-MS	Dehghan et al. (2012)
<i>Artemisia annua</i>	PCR	Artemisinin	HPLC	Ahlawat et al. (2012)
<i>Rehmannia glutinosa</i>	PCR analysis using <i>rol B</i> and <i>rol C</i> primers	Iridoid glycosides and phenylethanoid glycosides	HPLC-ESI-MS	Piateczak et al. (2012)
<i>Clitoria ternatea</i>	Southern blot hybridisation	Taraxerol	HPTLC	Swain et al. (2012)
<i>Panax quinquefolium</i>	PCR analysis	Ginsenosides	HPLC	Kochan et al. (2013)
<i>Scutellaria baicalensis</i>	PCR analysis	Resveratrol	HPLC	Lee et al. (2013)
<i>Dracocephalum kotschyi</i>	PCR detection of <i>rol C</i> and <i>aux1</i> genes	Rosmarinic acid	HPLC	Fattahi et al. (2013)
<i>Decalepis hamiltonii</i>	PCR analysis using <i>rol C</i>	2-Hydroxy-4-methoxybenzaldehyde	HPLC	Samyudurai et al. (2013)
<i>Hypericum perforatum</i>	PCR analysis using <i>rol B</i> primers	Xanthone	HPLC	Tusevski et al. (2013)
<i>Gentiana scabra</i>	PCR analysis using <i>rol B</i> and <i>rol C</i> primers	Loganic acid	HPLC	Huang et al. (2014)
<i>Astragalus membranaceus</i>	PCR amplification of <i>rol B</i> , <i>rol C</i> and <i>aux1</i> genes	Isoflavonoids	LC-MS/MS	Jiao et al. (2014)
<i>Rauwolfia serpentina</i>	PCR amplification of <i>rol B</i> primers	Reserpine	HPLC	Pandey et al. (2014)
<i>Portulaca oleracea</i>	PCR amplification of <i>rol B</i> primers	Dopamine	HPLC	Mohghadam et al. (2014)
<i>Polygonum multiflorum</i>	PCR and RT-PCR using <i>rol C</i> primers	Pyrogallol, hesperidin, naringenin and formononetin	UPLC	Thiruvengadam et al. (2014)

Table 1 (continued)

Plant species	Detection of gene transformation	Secondary metabolite obtained	Detection/quantification method	References
<i>Tripterygium wilfordii</i>	PCR analysis using <i>rol B</i> , <i>rol C</i> , <i>Aux1</i> , <i>VirG</i> and <i>VirD2</i> primers	Triptolidide and wilforine	HPLC	Zhu et al. (2014)
<i>Rhinacanthus nasutus</i>	PCR analysis and Southern hybridisation analysis	Rhinacanthin	HPLC	Cheruvathur et al. (2015)
<i>Cannabis sativa</i>	NM	Cannabinoids	HPLC and LC-MS	Frag and Kayser (2015)
<i>Stevia rebaudiana</i>	PCR detection of <i>rol B</i> and <i>rol C</i> genes	Chlorogenic acid	HPLC-MS and HPLC analysis	Fu et al. (2015)
<i>Isatis tinctoria</i>	PCR amplification of <i>rol B</i> , <i>rol C</i> and <i>aux1</i> genes	Bioactive alkaloids	LC-MS/MS	Gai et al. (2015a, b)
<i>Andrographis paniculata</i>	PCR analysis using <i>rol A</i> and <i>rol C</i> primers	Andrographolides	HPLC	Marvani et al. (2015)
<i>Gentiana dinarica</i>	GUS assay and PCR analysis	Xanthone	HPLC	Vinterhalter et al. (2015)
<i>Boerhaavia diffusa</i>	PCR analysis using <i>rol B</i> and <i>rol C</i> primers	Boeravinone B and eupalitin	HPLC	Gupta et al. (2016)
<i>Plumbago rosea</i>	NM	Plumbagin	HPLC	Jose et al. (2016)
<i>Gynemna sylvestre</i>	PCR and RT-PCR	Gymnemic acid	HP TLC and HPLC	Rajashakar et al. (2016)
<i>Abutilon indicum</i>	NM	Quercetin	Shinoda test, Zn-HCl reduction test and ferric chloride and TLC and HPLC	Sajjalagudiam and Paladugu (2016)
<i>Hypericum perforatum</i>	NM	Chlorogenic acid and 3- <i>p</i> -coumaroylquinic acid (quercitrin and quercetin isoquercetin), mangiferin	HPLC	Tusevski et al. (2016)
<i>Callerya speciosa</i>	PCR analysis using <i>rol B</i> and <i>rol C</i> primers, amplification and Southern blot	Polysaccharide	Phenol–sulphuric method	Yao et al. (2016)
<i>Artemisia vulgaris</i> and <i>Artemisia dracunculus</i>	NM	Artemisinin	HP TLC-MS	Drobot et al. (2017)
<i>Salvia runcinata</i>	RT-PCR and PCR analysis using <i>rol A</i> , <i>rol B</i> , <i>rol C</i> and <i>ags</i> primers	Caffeic acid	GC-MS	Figlan and Makunga (2017)
<i>Vitis vinifera</i> subsp. <i>sylvestris</i>	PCR detection of the <i>rol B</i> gene	Resveratrol	HPLC and TLC	Hossieni et al. (2017)
<i>Trifolium pratense</i>	PCR analysis using <i>rol A</i> primers	Isoflavones: daidzein, genistein, and biochanin A formononetin	HP TLC	Kumar et al. (2017)
<i>Withania somnifera</i>	PCR analysis using <i>rol B</i> and <i>rol C</i> primers	Withanolide	HPLC	Shahjahan et al. (2017)
<i>Salvia viridis</i>	PCR analysis using <i>aux1</i> , <i>aux2</i> , <i>rol B</i> and <i>rol C</i> primers	Rosmarinic acid	UPLC-PDA-ESI-MS	Grzegorzczak-Karolak et al. (2018)
<i>Ophiorrhiza mungos</i>	PCR analysis using <i>rol C</i> and <i>VirC</i> primers	Camptothecin	HPLC and LC-MSMS	Wetterauer et al. (2018)
<i>Sphagneticola calendulacea</i>	Transgenic HR selection via <i>GUS</i> staining analysis and PCR analysis	Wedelolactone	HP TLC	Kundu et al. (2018)
<i>Andrographis paniculata</i>	PCR analysis using a <i>rol C</i> primer	Andrographolide	HP TLC	Mahobia and Jha (2018)
<i>Linum flavum</i>	PCR analysis of <i>rol B</i> , <i>rol C</i>	6-Methoxy-podophyllotoxin, podophyllotoxin and deoxypodophyllotoxin	UPLC-HR-MS	Renouard et al. (2018)
<i>Pueraria candollei</i> var. <i>mirifica</i>	PCR analysis using a <i>rol A</i> primer	Deoxymiroestrol and isoflavonoids	ELISA	Udomsin et al. (2018)

**Table 1** (continued)

Plant species	Detection of gene transformation	Secondary metabolite obtained	Detection/quantification method	References
<i>Prosopis farcta</i>	PCR analysis using <i>rol C</i> and <i>VirD</i> primers	Flavonoids	LC/MS	Zafari et al. (2018)
<i>Ligularia fischeri</i> Turcz. f. <i>sptiformis</i>	PCR analysis using a <i>rol C</i> primer	Polyphenolic compounds	UHPTLC	Ansari et al. (2019)
<i>Silene linicola</i> C.C. Gmelin	Not mentioned	20-Hydroxyecdysone (20E), turkesterone and polygodin B	HPLC	Erist et al. (2019)
<i>Ferula pseudalliacea</i>	PCR analysis of the <i>rol B</i> gene	Farnesiferol B	HPTLC	Khazaei et al. (2019)
<i>Rehmannia elata</i>	RNA isolation and RT-PCR analysis	Verbascoside and isoverbascoside	UHPTLC	Piąteczak et al. (2019)
<i>Trigonella foenum-graecum</i>	PCR analysis using <i>rol B</i> primers	Steroidal saponenin	Gas liquid chromatography	Kohsari et al. (2020)
<i>Corylus avellana</i>	PCR analysis using a <i>rol C</i> primer	Paclitaxel	HPTLC	Parizi et al. (2020)

ELISA enzyme-linked immunosorbent assay, HPLC high-performance liquid chromatography, HPTLC high-performance thin-layer chromatography, LC-APCI-MS liquid chromatography–atmospheric pressure chemical ionisation–mass spectrometry, LC/MS liquid chromatography/mass spectrometry, MM not mentioned, PCR polymerase chain reaction, RT-PCR reverse transcriptase polymerase chain reaction, UPLC-HR-MS ultra-performance liquid chromatography–high-resolution mass spectrometry, UPLC-PDA-ESI-MS ultra-performance liquid chromatography–photodiode array–electrospray ionisation–mass spectrometry, UPLC ultra-performance liquid chromatography, UHPTLC ultra high-performance thin-layer chromatography

HR cultures mention the isolation of ajmaline, ajmalicine from *Rauvolfia micrantha* (Sudha et al. 2003), verbascoside from *Gmelina arborea* (Dhakulkar et al. 2005), sanguinarine, codeine from *Papaver somniferum* (Le Flem-Bonhomme et al. 2004) and coniferin from *Linum flavum* (Lin et al. 2003a). Recent research investigations have also led to the quantification of different phytochemicals like isoflavones from *Trifolium pratense* (Kumar et al. 2017), crypto tanshinone and tanshinone from *Perovskia abrotanoides* (Ebrahimi et al. 2017), withanolide from *Withania somnifera* (Shahjahan et al. 2017), andrographolides from *Andrographis paniculata* (Mahobia and Jha 2018), flavonoids from *Prosopis farcta* (Zafari et al. 2018), farnesiferol B from *Ferula pseudalliacea* (Khazaei et al. 2019), verbascoside and isoverbascoside from *Rehmannia elata* (Piąteczak et al. 2019) and steroidal saponenin from *Trigonella foenum-graecum* (Kohsari et al. 2020). All of these metabolites have various anti-cancerous, anti-arrhythmic, anti-hypertensive, anti-tumour and multiple other different medicinal properties. This enhancement in the production of different valuable secondary metabolites was accomplished by the introduction of a gene construct encoding an important protein (enzyme) required in the metabolic pathway of the chemical. In some cases, overexpression of the genes also led to the increase in metabolite production. Cultures were fast-growing and easy to maintain and synthesised more than one phytochemical.

### Study of gene function

The technique of manipulation of gene construct via which the desired transformation through *A. rhizogenes* is brought about could be further utilised for the studies of gene expression, gene silencing and differential promoter expression levels under different conditions. For example, a promoter induced by a glucocorticoid was utilised to produce the transformed HR cultures of *Catharanthus roseus*. In a glucocorticoid dexamethasone-supplemented medium, the promoter exhibited a reversible dose-regulated response (Hughes et al. 2002). Similarly, Preiszner et al. (2001) in their experimental investigations with HR cultures of soybean reported the differences in the response of the alcohol dehydrogenase promoter fused with the *GUS* gene to different treatments of cold temperature, abscisic acid, low oxygen stress and plant injury.

### Gene transfer technology employing *A. rhizogenes* as a vector

The system of binary vector of *A. rhizogenes* can be well utilised to integrate foreign genes, develop gene constructs and transfer them into different plant species. This technique has already been applied in case of *Stylosanthes* (Manners and Way 1989), potato (Visser et al. 1989), cucumber (Trulson et al. 1986) and different crops of Cruciferae (Christey and

Sinclair 1992). Co-integrated *Ri* plasmids with incorporated foreign genes are used for gene transfer in crops like tobacco (Comai et al. 1985), tomato (Morgan et al. 1987) and *Solanum* sp. (Davey et al. 1987). Some of the useful genes like jellyfish protein gene, anthocyanin gene, genes for GUS assay, reporter genes and selectable marker genes like *Hpt* and *NPT II* are transferred (Christey 1997).

### Encoding of proteins from related and unrelated taxa

Commercial utilisation of the HR cultures through insertion and gene expression of foreign genes and proteins has been done. Insertion of economically important genes from related or unrelated genera in the transformed root cultures has been achieved. It is noteworthy to mention that viral coat protein genes like that from grapevine mosaic virus were used to transform grapevine HR culture (Torregrosa and Bouquet 1997). Similarly, transformed white clover HR culture was produced upon the transfer of pea Lectin genes (Diaz et al. 1995).

### Metabolic engineering

Manoeuvring the genetic construction of the *Ri* plasmid T-DNA of HR-inducing bacteria via incorporation of alien genes between the TL and TR of the *Ri* plasmid that code for the enzymes of the concerned metabolic pathway and then transform the plant cells with this gene construct is metabolic engineering. This method has been lucratively exercised to enhance alkaloid biosynthesis in *Catharanthus roseus* and in different HR cultures of solanaceous plants (Palazon et al. 2003b; Moyano et al. 2003). Production of important biomolecules such as secreted embryonic alkaline phosphatase (SEAP) in human (Gaume et al. 2003), GFP and ricin toxin B (RTB) fusion proteins (from tobacco HR cultures; Medina-Bolivar et al. 2003) and accumulation of poly-3-hydroxybutyrate (from HR cultures of sugar beet; Menzel et al. 2003), solanoside glycoside (from HR culture of *Solanum khasianum*; Putalun et al. 2003), etc., are some of the notable examples mentioned in the different available literature.

### Biotransformation

Biotransformation deals with the conversion of naturally available phytochemicals to other biochemicals through structural changes in the original metabolite, employing plant biosystems in the process and thus creating novel and more useful biochemicals suited to the economic use of human beings. This leads to the production of second-generation pharmaceuticals which have enhanced pharmacokinetics, better solubility in biological systems and lesser toxicity. In this context, as per the review report of Banerjee et al. (2012), HR cultures have proven as the beneficial cultures for carrying out this process. These cultures provide low cost, genetic stability and multi-

enzyme biosynthetic potential for this process. The different types of biochemical reactions involved in this process in the cultures are hydroxylation, glycosylation, oxidation, condensation, hydrolysis, hydrogenation, acetylations, methylations, esterifications and isomerisation of various exogenously applied substrates as seen in the findings of Giri et al. (2001a) and Ishihara et al. (2003). The most commonly occurring biotransformation reaction is glucosylation or glycosylation. HR cultures of *Coleus forskohlii* effectively biotransformed the ethanol and methanol substrates into their respective  $\beta$ -D-ribohex-3-ulopyranosides and  $\beta$ -D-glucopyranosides (Li et al. 2003). Similarly, Chen et al. (2008) stated a region-selective glycosylation in HR cultures of *Panax ginseng* where glycosides along with glycosyl esters were produced from the two isomers of hydroxybenzoic acid. Reduction reactions were common in case of HR cultures of *Daucus carota* (Caron et al. 2005) and *Brassica napus* (Orden et al. 2006) with differential stoichiometry of their indigenous enzymes to the substrates. Apart from the above two reactions, HR cultures of four members from non-Asteraceae and six members from Asteraceae family exhibited a condensation reaction, producing the dimeric quinone, stilbequinone; though these reactions were rarer compared to the others. In this regard, Flores et al. (1994) reported that the addition of *Pythium aphanidermatum* elicitors to the cultures biotransformed BHT to stilbequinone. Divergence in reaction responses depend upon the mother plant species that is used to initiate the culture. For instance, in the findings of Nunes et al. (2009), HR cultures of *Levisticum officinale* showed differential reaction responses to menthol and geraniol substrates. The HR cultures exhibit acetylation, isomerisation, reduction, cyclisation and oxidation reactions to the addition of geraniol whereas no reaction was seen to methanol addition. Substrates reduced were mainly carbonyl functional group conjugated with aromatic ring.

Apart from the various reaction types involved, other laboratory factors affect the efficiency of biotransformation process. The HR cultures comprising the plant families, viz. Solanaceae, Asteraceae, Campanulaceae and Araliaceae, were more responsive to biotransformation. It was mentioned in the reports that responsiveness to biotransformation was more pronounced at species level than at family level (reviewed in reports of Banerjee et al. 2012). Interestingly, it was pointed out by Nunes et al. (2009) and Faria et al. (2009) that the HR cultures of *Levisticum officinale* and *Anethum graveolens*, having the same taxonomic origin (same family), show differential responses of biotransformation to the same substrate. Considering the strain of the bacterium *A. rhizogenes*, the strains A4, ATCC 15834 and LBA 9402 proved to be more effective than others. Regarding the basal media for biotransformation studies, Murashige and Skoog (1962) medium is the preferred choice. Sucrose was used as a carbon source. In case of *Datura tabula*, favourable results in biotransforming *p*-hydroxybenzyl alcohol into gastrodin were



obtained with supplementation of media with salicylic acid (Peng et al. 2008). Flores et al. (1994) reported 20 h as the time taken for the reactions to complete; though in the findings of Peng et al. (2008), the duration of up to 25 days was reported. It was reported that in most of the cases, the desired products were obtained from the media as well as the roots.

## Phytoremediation

The utilisation of plants to tackle environmental pollution by the accumulation and absorption of different heavy metal ions or the polluting contaminants from the substratum and to alter those into nontoxic compounds is called phytoremediation (Suresh and Ravishankar 2004). Through recent research, it has been found that apart from the different in vivo available phytoremediator plants, the transgenically developed HR cultures are also efficient in this detoxification process. In some earlier reports (Agostini et al. 2003; Gujarathi et al. 2005), it is mentioned that different crops like *Helianthus annuus*, *Brassica juncea* and *Cichorium intybus* and their respective HR cultures are efficient in cleansing up pesticides like dichlorodiphenyltrichloroethane (DDT), 2,4-dichlorophenol (2,4-DPC) and other industrial wastes.

There are different reports providing accounts of the phytoremediation technology using HR cultures. The HR is regarded as a model system since this technology allows to study the cellular responses, cell signalling, gene physiological studies and cellular abilities during countering the toxins. Not only this, HR cultures could be utilised in phytomining operations to obtain metal-enriched product from the plant biomass (Boominathan et al. 2004). Under this system, translocation of pollutants to upper parts of the plants do not take place. Quicker proliferation rates and stable genotypic and phenotypic performance of these cultures further make them favourable choices over other cell cultures. Previously mentioned, plant species like *Brassica*, *Helianthus annuus* and *Alyssum* are good bioaccumulators that provide valuable information regarding heavy metal ion accumulation in the rhizosphere and their subsequent management (Eapen et al. 2003; Nedelkoska and Doran 2001; Soudek et al. 2006). To deal with the inorganic and organic pollutants, the genetic architecture of the plants with respect to their ability is altered. This genetic change could be brought about by enhancing the intrinsic proteins that affect the ion accumulation and translocation. This is brought by fortification in the gene expression or by incorporation of related novel genes through biotechnology. This transformation is brought about using suitable gene constructs with plasmids that are easy to manipulate.

Citing an interesting example, Rodríguez-Llorente et al. (2012) reported the utilisation of transgenic HR culture in *Arabidopsis thaliana* to phytoremediate inorganic pollutants through the expression of Cu-binding periplasmic protein (CopC). The organic pollutants were countered via in vitro

HR culture of *Atropa belladonna* showing the expression of a rabbit P4502E1 enzyme (Banerjee et al. 2002). Similar investigations were reported in experimental results of Wevar Oller et al. (2005) as well as Sosa Alderete et al. (2009) wherein tobacco and tomato HR cultures expressed a basic peroxidase enzyme to detoxify phenolic compounds more efficiently than natural-type HR. Thus, the concept ‘supertransgenic plants through multi-transgene strategy’ was put forward (Macek et al. 2008). Hence, the potential of HR culture for further biotechnological interventions is explored.

## Production of novel compounds or proteins

An accrual of conjugates of flavonoid glucoside in the HR cultures of *Scutellaria baicalensis* Georgi. was detected when compared to the normally occurring conjugates of glucose as observed in the normal root cultures (Nishikawa and Ishimaru 1997).

## Bringing out structural changes in the metabolite

Incorporation and subsequent expression of *Antirrhinum* dihydroflavonol genes in the HR cultures of *Lotus corniculatus* led to changes in the structure of condensed tannin and their increased accumulation in the HR (Bavage et al. 1997). Similar instances of improved metabolite production through genetic changes in the metabolism were mentioned in the reports of Berlin et al. (1993) wherein the *TDC* gene segment from periwinkle (*Catharanthus roseus*) was overexpressed in the HR cultures of *Peganum harmala* that resulted in increased TDC activity. Hashimoto et al. (1993) testified that the constitutive expression of the *H6H* gene transferred from *Hyoscyamus niger* to *Atropa belladonna* led to the conversion of hyoscyamine to scopolamine in the root tissues.

## Whole plant regeneration

It has been reviewed by Hu and Du (2006) that through the addition of appropriate PGRs like 2,4-dichlorophenoxyacetic acid (2,4-D),  $\alpha$ -naphthaleneacetic acid (NAA) and 6-benzylaminopurine (BAP) in the medium, the HR could be induced to produce shoots and somatic embryos. For instance, it was reported that the addition of 7.5–10 mg 2,4-D into the media led to the generation of somatic embryos in the HR cultures of *Astragalus sinicus* (Cho and Wildholm 2002).

## Promoting root formation in vegetative propagation

For the successful perpetuation through vegetative propagation, rooting is an important aspect. So, HR culture technology could be utilised to promote rooting in many of the recalcitrant crops like apple, peaches, olive, *Pinus* spp. and *Larix* spp. (McAfee et al. 1993; Bosselut et al. 2011). This is brought

about by the introduction of the Ri plasmid ‘*rol*’ genes of *A. rhizogenes* into the host plant genome (Rugini and Mariotti 1991).

### Study of the rhizosphere and culturing of beneficial obligate parasites

By developing an efficient root system in different plants, the study of root morphology, functions and rhizosphere effects as well as plant–microorganism interactions can be performed. Functions and the role of some secondary phytochemicals in influencing the soil bacteria could also be studied. HR cultures can be utilised for the culturing of beneficial fungi like the mycorrhiza. Some of the examples mentioned are *Glomus mosseae* and *Gigaspora margarita* fungi on the HR of *Convolvulus sepium* L. (Mugnier and Musse 1987). These root cultures can also be used for host–pathogen interaction especially the soil-borne pathogens. Cai et al. (1997) were successful in their experiments on developing resistance in sugar beet to beet cyst nematode (*Heterodera schachtii* Schmidt) by transforming susceptible sugar beet HR cultures with the *Hs<sub>r</sub><sup>pro1</sup>* gene. Further investigations regarding the outcomes of different other pesticides and chemical on roots and root-interacting microorganisms (both beneficial and harmful) can be done (reviewed by Eapen and Mitra 2001).

### Scaling-up process

For up-scaled commercialisation of HR cultures for pharmaceutical implementations, a scaling-up process is important. There has been significant progress in the field of scaling-up process of the HR biosystems with respect to their economic uplift and industry-based research and development. A varied number of bioreactors have surfaced with proficient management facilities and with improved scientific outlook. The exclusive aim of these commercial exploitations is to maximise the benefits derived from the economically invaluable phytochemicals which possess immense ethnobotanical and therapeutic uses. Conventional fermentors are rather unsuitable. There are certain important factors to be kept in mind regarding the setting up of HR bioreactor systems. It has to be borne in mind that prolonged sustenance of cultures in reactor units is vital to the profitable harvest of biochemicals. Various results from different workers show that proper aeration of the culture medium (in case of liquid cultures) is crucial for better circulation, uptake of nutrients and effectual economic product biosynthesis as it optimises oxygen–carbon dioxide balance (Bhojwani and Razdan 1996). HR cultures thrive better in suitable support systems. Varied resources put into use are polyurethane foam (Steingroewer et al. 2013), nylon mesh (Gangopadhyay et al. 2011) and stainless steel base (Srivastava and Srivastava 2012). Angelini et al. (2011)

mention the use of nylon mesh in HR bioreactors for phytoremediation studies.

Hence, the following must be kept in mind: distinctive morphological structure of HR, oxygen requirements, etc.; different bioreactors like air-sparged reactors (Taya et al. 1989; Rodriguez-Mendiola et al. 1991); nutrient sprinkle bioreactor (Kuzma et al. 2009); stirred tank reactors (Davioud et al. 1989; Kondo et al. 1989; Hilton and Rhodes 1990; Cardillo et al. 2010; Rahimi et al. 2012); mechanically driven bioreactors, viz. rotary drum reactors and turbine blade reactors (Kondo et al. 1989; Mitchell et al. 2006); immobilised bioreactors like trickle-bed reactors (Flores and Curtis 1992); nutrient mist bioreactor (Huang et al. 2004); pneumatically driven bioreactors, viz. airlift balloon bioreactors (Ali et al. 2007); bubble column reactors (Hilton and Rhodes 1990; Rodriguez-Mendiola et al. 1991; Kwok and Doran 1995; Ludwig-Müller et al. 2008; Georgiev et al. 2012); etc. However, the response to these bioreactors is species specific. For instance, HR cultures of *Artemisia annua* exhibit sustenance for longer period in inner-loop airlift bioreactor (Liu et al. 1998). Apart from this, airlift reactors (in case of *Solanum chrysotrichum*) and mist reactors are also used (Caspeta et al. 2005). In the experimental investigations of Ramakrishnan and Curtis (2004) and Suresh et al. (2005), it was stated that in mist reactors, HR cultures were hung to a mesh support, thereby reducing the amount of culture media and also obtaining the desired phytochemical in concentrated form. The latter method is widely used by the ROOTec Company. As a cost-effective approach, ‘rhizosecretion’ of the phytochemicals could be achieved by integration of the plant-based hydroponic system with the HR culture system (Gaume et al. 2003).

Computer graphics–based mathematical simulation modelling tactics are deployed to address the various culture-related issues of HR in bioreactors. Srivastava and Srivastava (2006) opined that this mathematical calculative strategy can greatly help researchers in finding the best possible combination of micronutrients and macronutrients for HR growth in bioreactors, leading to time economy and averting resource wastage. Under practical conditions in general due to the dynamicity of the plant cellular organs, exact estimation of the growth kinetics is not possible. Hence to maximise precision, different workers have put forward different models, viz. Patra and Srivastava (2015) in *Artemisia annua* and Thakore et al. (2015) in *Catharanthus roseus*. Mairet et al. (2010) in their investigative reports have recommended different models to characterise HR culture, viz. branching model (based on root differentiation), metabolic model (based on differential metabolic processes) and oxygen-limited growth kinetic model (based on oxygen concentration in the culture).

Of late, bioreactors with novel prototypes have been put into use to improvise the pharmaceutical applications of HR culture as secondary biochemical resources. Some of the

reactor systems worth mentioning are hydraulically driven bioreactors—wave-mixed bioreactors (Huang and McDonald 2012), temporary immersion bioreactors (Ducos et al. 2009), microbioreactors (Diao et al. 2008), ebb-and-flow regime bioreactors (Cuello and Yue 2008) and slug bubble bioreactors (Kantarci et al. 2005).

## Constraints encountered

Despite many lucrative advantages, HR culture technology is fraught with many problems and hindrances (Ibañez et al. 2016). General problems encountered during the culturing are as follows.

### Probable chromosomal aberrations

Progressive reduction in the chromosome numbers in cultures of *Onobrychis viciifolia* Scop. was noticed over a subculturing period ranging from 4 to 8 months. The chromosome number of normal somatic cells ( $2n = 28$ ) was found in 4.1% of cells (Hu and Du 2006).

### Genetic changes leading to gene suppression

Silencing of gene expression at later stages of subculturing in tryptophan decarboxylase (TDC) and strictosidine synthase (STR) transformed *Cinchona officinalis* L. cultures despite earlier prolific expression levels (Greerlings et al. 1999). An increase in the copy number of transgenes also may lead to poor gene expression levels, leading to less harvest of a desired metabolite as noticed in HR induction experiments of *Catharanthus roseus* transformed with hamster HMGR cDNA producing higher campesterol and serpentine but altered levels of ajmaline and catharanthine amongst the clones (Ayora-Talavera et al. 2002).

### Regenerants showing morphological alterations

As per the available literature, the transgenic regenerants exhibit changes like wrinkled and variegated leaves, plagiotrophic rooting, altered apical dominance and poor plant stature (Tepfer 1984; Tayler et al. 1985; Cardarelli et al. 1987; Spano et al. 1988; Hamamoto et al. 1990). Also, leaf asymmetry and shortened shoot length have also been reported. These changes may be genetically occurring due to inaccuracy in transgene insertion and somaclonal variations (Han et al. 1993).

## Overexpression of gene might not always give the expected exponential biochemical production

This condition was noticed in the experimental findings of Koehle et al. (2002) in case of HR cultures of *Lithospermum erythrorhizon* Sieb. showing no further increment in shikonin production.

## Related species exhibit differential production of secondary metabolite

HR cultures of two related genera (*Datura metel* and *Hyoscyamus muticus*) produce differential tropane alkaloids (Moyano et al. 2003). Also, the background genotypic constitution of the plants may impinge on the transgene expression, as seen in the HR cultures of *L. corniculatus* (Carron et al. 1994).

## Problems faced during phytoremediation

Problems of the HR cultures to tackle the fluctuating environmental changes in view of the quantity, volume and form of pollutants were generated out into the environment (Khandare and Govindwar 2015). Also, the results of this technique in field level differ significantly compared to the laboratory conditions (Angelini et al. 2011). Lack of appropriate infrastructure and skilled personnel is also a problem for large-scale operation.

## Application with cutting-edge technologies

Over recent years, transcriptome sequencing has surfaced as an innovative biotechnological advancement in improvising the field of HR culture technology with respect to the illumination of the complex internal biosynthetic processes of phytometabolite production in the HR cultures, thereby facilitating their establishment, biofortification and enhanced secondary metabolite extraction. Bolger et al. (2014) and Chaudhary and Sharma (2016) in their reports mention about the boom in the scientific technology due to the advent of these next-generation technologies of polynucleotide sequencing. HR cultures of different plants of medicinal value have been analysed using this technology such as *Panax ginseng* (Cao et al. 2015), *Astragalus membranaceus* (Tuan et al. 2015), *Salvia miltiorrhiza* (Gao et al. 2014; Xu et al. 2015) and *Rehmannia glutinosa* (Wang et al. 2017). The generally used NGS methods were Illumina/Solexa and Roche 454. From the investigations of Yamazaki et al. (2013) in *Ophiorrhiza pumila* HR culture, the information generated from the sequencing of the cellular transcripts using Illumina/Solexa revealed the metabolic mechanism of camptothecin production. Similarly, Illumina techniques

coupled with RT-qPCR were employed in *Catharanthus roseus* to expound the effects of overexpression of anthranilate synthase in the HR culture (Sun et al. 2016). In *Centella asiatica*, it was found that cytochrome P450 hydroxylase and carboxylase are involved in the production of metabolic intermediates which ultimately yield the products asiaticosides and madecassosides (in reports of Kim et al. 2014). In view of this, transcriptome sequencing provides itself as an innovative way out for studying the various metabolism pathways of phytometabolite production in the HR cultures in view of its high-throughput data generation and effective and quicker characterisation of transcriptomic information.

The scaling-up process of the laboratory-based HR cultures requires efficient and meticulous monitoring and supervision of the cultures in the bioreactors so as to harness the invaluable secondary phytobiometabolites. Effective utilisation of the HR cultures under traditional methods are arduous, time consuming and prone to mismanagement. Hence, in sight of this, modern methods based on in silico simulation modelling are developed to speed up and ease out the pharmaceutical utilisations of the HR cultures. Amongst the various recently published works, different models utilised for HR culture are Box–Behnken design (BBD) in *Isatis tinctoria* for secondary metabolite studies (Gai et al. 2015a, b), artificial neural network systems in *Rauwolfia serpentina* (Mehrotra et al. 2013) for biosystem productivity studies and in *Artemisia annua* (Osama et al. 2013) for evaluation studies on the influences of different bioreactors on HR growth and agent-based modelling in *Beta vulgaris* to study the root morphological parameters (Lenk et al. 2014). Most of the modelling studies aim at evaluation of various growth factors and subsequent setting up of an optimised protocol for HR cultures in bioreactors. In *Catharanthus roseus*, statistical design was used to study media condition effects on HR development (Bhadra and Shanks 1995). Similar mathematical modelling method was practised in *Azadirachta indica* HR to infer about the biomass growth of HR culture affected by differential oxygen and mass transfer rates (Palavalli et al. 2012). Morphological assessments centred on root branching (Kim et al. 1995) and root elongation (Bastian et al. 2008) studies were also done. Regulation of mist in the mist reactors is a crucial factor. Both longer and shorter durations of mist lead to nutrient choking. Ranjan et al. (2009), in their investigations, formulated a mathematical way-out model to optimise the mist bioreactor specifications. An up-to-date response surface methodology (RSM) technology combining statistical and mathematical method has been developed. In the published reports of Amdoun et al. (2009, 2010), this modelling tool finds its application in *Datura stramonium* HR culture for estimating the influences of media composition and metal ion media additives for hyoscyamine enhancement. Another dependable and noteworthy technique is the genetic algorithm technology. Arab et al. (2016) attested in their reports that this computer science–based methodology

utilises the principle of survival of the fittest and natural selection which is experimentally achieved through stochastic sampling. Using population parameters, this heuristic technique finds remedies to problems of HR biosystem growth limitations such as media optimisation and root biomass–affecting factors. In silico image analysis tool facilitates researchers to develop a two-dimensional image diagram of HR. In this context, a number of software are available such as WinRHIZO, ROOTEDGE and PetriCam. Findings of Flavel et al. (2017) demonstrate an improvement in the precision of their experiments upon using this tool. Lenk et al. (2012) have testified that by using this technology, the secondary phytobiometabolite production can be determined through root morphology surveillance. Thus, it is seen that these computer-defined approaches help researchers in studying the growth patterns and morpho-physiological responses of the HR systems.

Genome editing has become more lucrative in recent times with the discovery of CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated nuclease 9) technology. This biotechnological tool along with metabolic engineering has found profitable utilisations in HR cultures, enabling researchers to study the gene functions and related biometabolite production pathways. Published results of Ron et al. (2014) mentioned that genetic architecture of HR cultures of tomato was amended, employing this technique, wherein varied deletion and insertion mutations were observed in the *SHR* (*SHORTROOT*) gene which led to phenotypic changes in the HR. Similar gene-editing exploits were carried out in soybean *SHR* and *FE12* genes present in situ along with foreign *bar* gene segment (Cai et al. 2015). Jacobs et al. (2015) in their findings in soybean state that this genetic engineering tool can also be applied to make amends in the genes in homeologous chromosomes in polyploids. The target gene *CPS1* in *Salvia miltiorrhiza* was metabolically engineered through CRISPR/Cas9 using AtU6-26SK, 35S-Cas9-SK and pCambia1300 vectors (Li et al. 2017).

## Conclusion and prospects

HR culture technology has been developed into an exciting biotechnological tool for researchers. Despite the occurrence of problems like chromosomal changes and fluctuating harvest of desired biochemical, the cultures are easily manageable, genetically stable than the cell suspension cultures and fast proliferating and provide a lot of pharmaceutical exploration. It also provides for the protection of the plants of medicinal value with respect to their demand for the biosynthesis of invaluable medicinal products by acting as an effectual way out for the secondary metabolite production. Regarding the commercial approaches, a more scientific outlook for cost-

effectiveness and sustained production is required. A lot of research and investigation have already undergone in this concerned sector of biotechnology spanning over the past 25 years. Various aspects like the metabolic engineering, large-scale secondary metabolite production and their enhancement through elicitation studies, studies on host–microorganism interactions through roots, genetic transformation, applying techniques of phytoremediation and biotransformation to produce novel biomolecules, utilising novel biotechnological tools like transcriptome sequencing studies, in silico simulation modelling technologies, mathematical modelling for HR biosystem studies and CRISPR–Cas9 technology for enhanced phytometabolite synthesis were dealt with. Despite extensive research, a lot still requires to be explored to extract the wholesome prospects of HR cultures for crop improvement.

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## Compliance with ethical standards

**Conflict of interest** The authors declare that they have no conflict of interest.

**Ethical approval** This article does not contain any studies with human participants or animals performed by any of the authors.

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